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How to Grow Different Crystal Structures using the Same Virus

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We explore how one might grow a crystal structure the way one folds a protein. Not only are proteins chemically heterogeneous, they interact via a hierarchy of interactions (electrostatic, hydrophobic, H-bonding, chaperones, and so on) at different time scales. It is currently believed that this multiplicity of interactions leads to the famous funnel-shaped “free-energy landscape” with many local free-energy minima that correspond to a large number of structural states. Being able to rationally and reproducibly navigate through the free-energy funnel will open the possibility of making a broad range of new structures. FCC is the global free-energy minimized crystal structure for ensembles of essentially all spherical objects that interact via isotropic potentials. However, by using bacteriophage viruses (MS2 and Qbeta, ~28 nm diameter) interacting via two prototypical principles of attraction, we can make this free-energy minimum almost irrelevant. Not only can we reproducibly grow face-centered cubic and hexagonal close-packed structures, we can also grow tetragonal-centered structures and unanticipated layered phases. We investigate these systems using a combination of high-resolution synchrotron X-ray scattering and molecular dynamics simulations.